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1600

RAW SEQUENCE LISTING   DATE: 06/12/2003
PATENT APPLICATION: US/09/765,061D   TIME: 09:02:28

Input Set : A:\UTHou-16UTL 79-88.ST25.txt
Output Set: N:\CRF4\06122003\I765061D.raw

```
 3 <110> APPLICANT: The Board of Regents of the University of Texas System
 5 <120> TITLE OF INVENTION: MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE
LEBER
 6       CONGENITAL AMAUROSIS (LCA4)
 8 <130> FILE REFERENCE: 96606/16UTL
10 <140> CURRENT APPLICATION NUMBER: 09/765,061D
11 <141> CURRENT FILING DATE: 2001-01-17
13 <150> PRIOR APPLICATION NUMBER: 60/331362
14 <151> PRIOR FILING DATE: 2001-01-04
16 <160> NUMBER OF SEQ ID NOS: 10 additional sequences, Seq. Nos. 79-88
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 79
21 <211> LENGTH: 34
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (1)..(34)
29 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
30       Residues 11-34 are the intronic sequence
32 <400> SEQUENCE: 79
33 cggatcccga gtgagtgggg ccctccggag caga                                    34
36 <210> SEQ ID NO: 80
37 <211> LENGTH: 35
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (1)..(35)
45 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
46       and Residues 26-35 are the exonic sequence.
48 <400> SEQUENCE: 80
49 cagagtgcac cgtctcggtg actaggtgat ctttc                                   35
52 <210> SEQ ID NO: 81
53 <211> LENGTH: 35
54 <212> TYPE: DNA
55 <213> ORGANISM: Homo sapiens
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (1)..(35)
61 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
62       Residues 11-35 are the intronic sequence
64 <400> SEQUENCE: 81
65 csacaccatc gtaagtaggc cctgcgcgcc tgtct                                   35
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Handwritten annotations: Does Not Comply / Corrected Diskette Needed. invalid, per 1.825 d Sequence Rules. "Any amendment to the paper copy of the 'Sequence Listing'... must be accompanied by a substitute copy of the computer readable form ... including all previously submitted data..." insert Sequences 1-78 from previously submitted CRF. a Sequence Listing must begin with Sequence 1

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 69 <211> LENGTH: 35
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Homo sapiens
 74 <220> FEATURE:
 75 <221> NAME/KEY: misc_feature
 76 <222> LOCATION: (1)..(35)
 77 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
 78       and Residues 26-35 are the exonic sequence.
 80 <400> SEQUENCE: 82
 81 gccatccatc cgtttatccc cacagcacac ggggg                           35
 84 <210> SEQ ID NO: 83
 85 <211> LENGTH: 35
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Homo sapiens
 90 <220> FEATURE:
 91 <221> NAME/KEY: misc_feature
 92 <222> LOCATION: (1)..(35)
 93 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
 94       Residues 11-35 are the intronic sequence
 96 <400> SEQUENCE: 83
 97 gctgctgcag gtggggctgg ggttggcagg gctgg                           35
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101 <211> LENGTH: 35
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
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108 <222> LOCATION: (1)..(35)
109 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
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110       and Residues 26-35 are the exonic sequence.
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113 cactgacctg cagctctggg gccaggttga tgccc                           35
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118 <212> TYPE: DNA
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122 <220> FEATURE:
123 <221> NAME/KEY: misc_feature
124 <222> LOCATION: (1)..(35)
125 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
126       Residues 11-35 are the intronic sequence
128 <400> SEQUENCE: 85
129 gcagaccaag gtcagaggcc gctggccacg gggtg                           35
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134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
138 <220> FEATURE:
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140 <222> LOCATION: (1)..(35)
141 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
142       and Residues 26-35 are the exonic sequence.
144 <400> SEQUENCE: 86
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149 <211> LENGTH: 35
150 <212> TYPE: DNA
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154 <220> FEATURE:
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156 <222> LOCATION: (1)..(35)
157 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
158       Residues 11-35 are the intronic sequence
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165 <211> LENGTH: 35
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
170 <220> FEATURE:
171 <221> NAME/KEY: misc_feature
172 <222> LOCATION: (1)..(35)
173 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
174       and Residues 26-35 are the exonic sequence.
176 <400> SEQUENCE: 88
177 gctggatgct ccctgctccc cacaggcatc gtgaa                              35
```

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